

1 GCTGTGGGAA CCTCTCCACG CGCAGCAACT CAGCCAAACGA TTTCTGATAG ATTTTGGGA GTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC  
CGACACCCCTT GGAGAGGTGC GCGTGTCTGA GTGGGTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACCTCCTC GCGAAGGATG

101 CGTTAGGGAA CTCTGGGAC AGAGCGCCCC GCGCCCTCTGA TGGCCGAGGC AGSGTGGAC CCAGGACCCA GGACGGCTC GGAACCCATA CCATGGCCCCG  
GCAATCCCTT GAGACCCCTG TCTCGGGGG CCGGGGACT ACCGGCTCCG TCCACGCTG GGTCTGGGT CCTGCGGAG CCCTGGGTAT GGTACCGGGC  
MetalArg

201 GATCCCCAAG ACCCTAAAGT TCGTCTCGT CATCTGCTG GTCTGCTGC CAGTCTAGC TTACTCTGCC ACCACTGCC GCGAGGAGGA AGTTCCCCAG  
CTAGGGGTTT TGGGATTCA AGCAGCAGCA GTAGCAGCG CAGGACGACG GTACAGATCG AATGAGACGG TGGTGACGG CCGTCTCCT TCAAGGGGTC

4 IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluG l uValProGln

301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCACGAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA  
GTCTGTCACC GGGGTGTCGT TGTCTCCGT TCGAAGTTCC CCCTCCTCAC AGGTCTCCT AGAGTATCTA GTCTGTATG ACCTGGACA TTGGGGCAGT

37 GlnThrVala laProGlnG l nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArg s erGluHisth rGlyAlaCy s AsnProCysThr

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTGTAAATC AGATCAAAA CATAAAAGTT CCTGCACCAT  
GTCTCCACA CCTAATGTGG TTGCGAAGGT TGTACTTGG AAGAACGAAG GTTACATGTC AACATTAG TCTAGTTTTT GTATTTTCAA GGACGTGTA

71 GluGlyVa laspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAGA AGGCACCTTC CGGAATGAAA ACTCCGAGA GATGTGCCG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC  
CTGGTCTCTG TGTACACAG TCACATTCT TCGTGAAG GCCTTACTTT TGAGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCTTCAG

104 ThrArgAsp ThrValCy sG l nCysLysG l uGlyThrPhe ArgAsnGluA snSerProG l uMetCysArg LysCysSerA rgCysProSe rGlyGluVal

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTG AAACCCGAGC TGCTGAAGAG ACAATGAACA  
GTTACAGTCAAT TAAATGCAG GACCTACTA TAGGTACACAC AACTTCTTAA ACCACGGTTA CCGTGACACC TTTGGGGTCG ACGACTTCTC TGTACTTGT

137 GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

701 CCAGCCCGGG GACTCCTGCC CCAGCTGCTG CAGACACAGC CCAGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG  
GGTCGGGGCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGTGTCG GGTCCCTGAG GACGGGGTCG ACGACTTCTC TGTACTGTTT GGTGCGGGCC

171 SerProG l yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly

FIG. 1A-1

**FIG. 1A-2**

-40

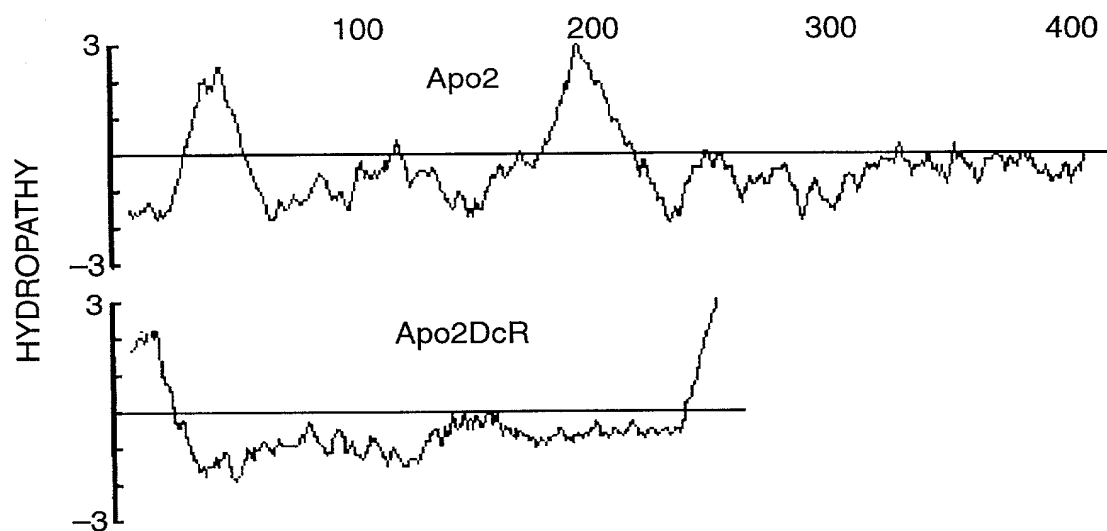
**FIG. 1B-1**

[illegible]

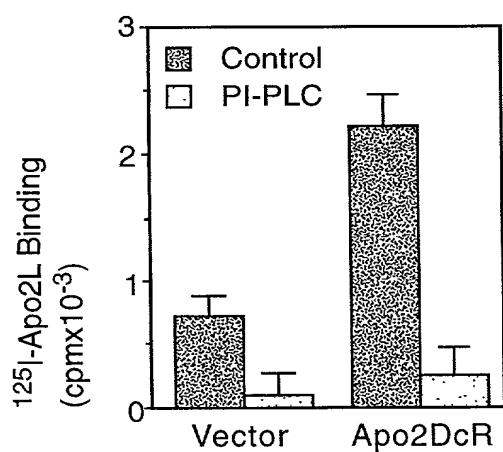
**FIG. 1B-2**

Apo2	1	-----MEQRGQNAFAASGARRRHGPGPREARGARPGRLVPKTLVL
Apo2DcR	1	-----MARIPKTLKEFVV
DR4	51	GRGALPTSMGQHGPSARARAGRAPGFRPAREASPRLRVHKTFKFVVQVL
Apo2	41	VVAAVLLLVSAESALITQODLAPQORAAPOOKRSSPSEGLCPPGHHISED
Apo2DcR	13	VIVAVLLPVLAYSATTAQEEVPQOTVAPQOQRHSFKGEECPAGSHRSEH
DR4	101	LQVVPSSAATIK-----LHDQSIGTQOWEHSPLGELCPPGSHRSEH
Apo2	91	GRDCISCKYGGDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQCE
Apo2DcR	63	TGACNPECTEGVDYTNASNNEPSCFCTVCKSDQKHSSCTMTRDTVCQCK
DR4	142	PGACNRCTEGVGYTNASNNEFACLPCTACKSDEEERSPCTTTRNTACQCK
Apo2	141	EGTFREEDSPEMCRKCRTGCPRGMVKVGDCPTWSDIECVHKE-----
Apo2DcR	113	EGTFRNENSPEMCRKCSR-CPSSGEVQVSNCTSWDDIQCVE-EFGANATVE
DR4	192	EGTFRNDNSAEMCRKCSTGCPRGMVKVKDCTPWSIDIECVHKE-----
Apo2		-----
Apo2DcR	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4		-----
Apo2	183	-----SGIILIGVTVAAVVLLIVAVEV----
Apo2DcR	211	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIIVLLIVLLIVFV
DR4	234	-----SGNGHNIWVILLVVTLVVPILLIVAV-LIVC
Apo2	203	CKSLWKKVLPYLKGICSGGGGDPFRVDRSSQRPGAEDNVLNEIVSILQP
DR4	262	CCIGSGCGDPEKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS
Apo2	253	TQVPEQEMEVOEPAEPTGVNMLSPGESEHLLPAAEAERSQRRRLVLPANE
DR4	312	----EQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRLVLPANG
Apo2	303	GDPTEITLRQCFDDFADLVFFDSWEFLMRKLGIMDNEIKVAKAEAAAGH--R
DR4	358	ADPTETIMLFEDKFAINIVFFDSWDQLMRQLDLTKNEIDVVRAGTAGP--G
Apo3/DR3	338	VMDAVPARRWKEFVRTLGLREAEIEAVEVEI-GRF-R
TNFR1	322	VVENVPPLRWKEFVRRGLSDHEIDRIELON-GRCLR
CD95	220	IAGVHTLSQVKGFVRKNGVNEAKIDEIKNDN-VQDTA
Apo2	351	*DILYIMLIKWVNKTGR-DASVHTLLDALETLGERLAKOKIEDHLLSSGKF
DR4	406	*DALYAMLKQVNKTGR-NASIHITLLDALERMEEERHAKKIQDLLVDSGKF
Apo3/DR3	374	*DQYEMLKRWRRQQQP---AGLGAVYAALERMGLDGCVEDLRS
TNFR1	358	EAQYSMLATWRRRTERRREATLELLGRVLRDMDLGLEDIEE
CD95	256	EQKVQLLRNWHQLHGKKEAY-DTLIKDLKANLCTLAEKIQ
Apo2	400	MYLEGNADSALS
DR4	455	IYLEDGTGSAVSLE

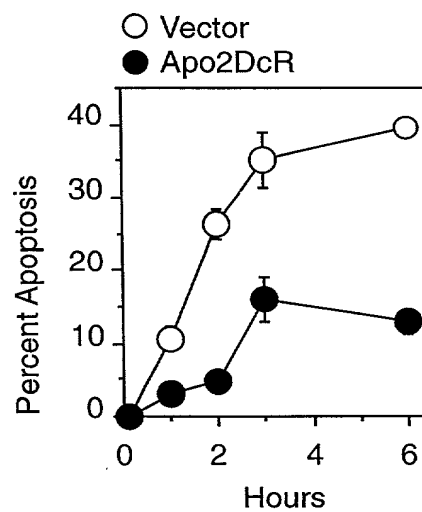
**FIG. 2**



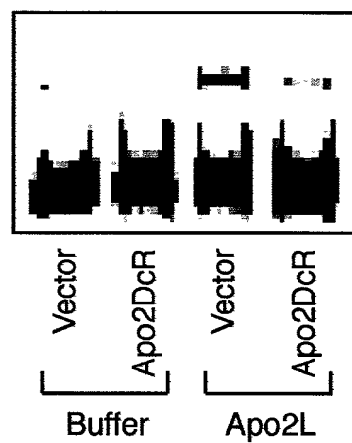
**FIG.\_3**



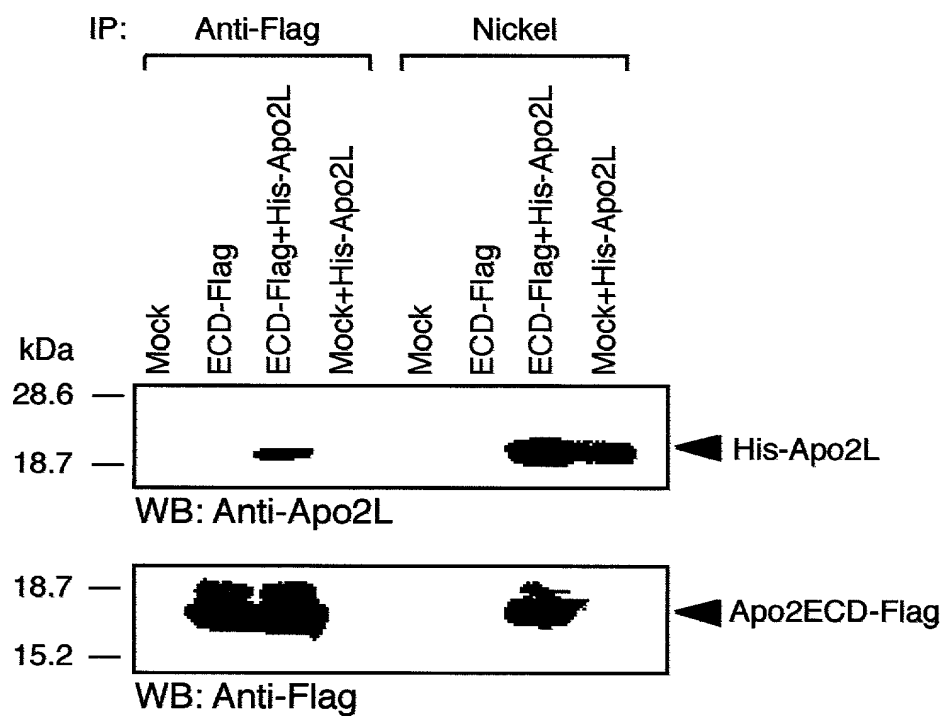
**FIG.\_4**



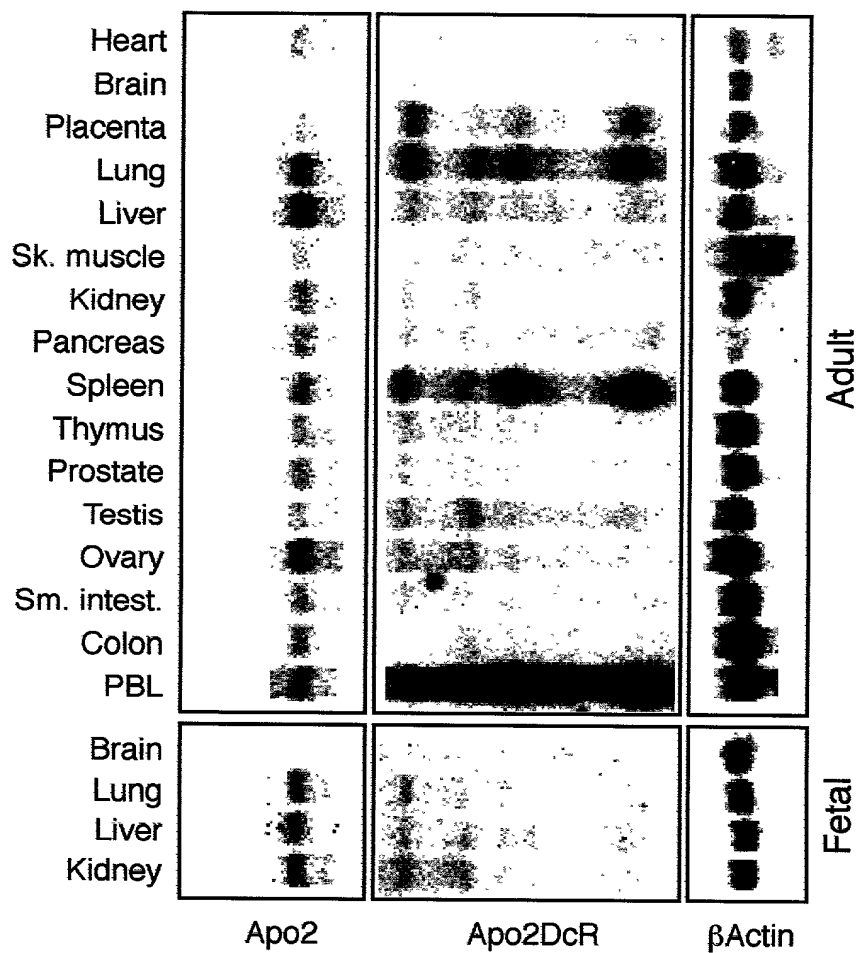
**FIG.\_5**



**FIG.\_6**



**FIG.\_10**



**FIG. 7**

+

1 CCCACGGGTC CGCATAAATC AGCAGCGGGC CGGAGAACCC CGCAATCTCT GCGCCACAA ATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAC  
GGGTGGCGAG CGTATTAG TCGTGGCGCG GCCTCTGGG CGGTAGAGA CCGGGGTCTT TTAATGGCT GCTACGGGCT AGATGAAATT CCCGACTTTC

101 CCACGGGGCT GAGAGACTAT AAGAGCGTTC CCTACGGCCA TGAACAACG GGGACAGAAC GCCCGGGCG CTTCCGGGGC CCGGAAAAGG CACGGCCCCAG  
GGTGGCCCGA CTCTCTGATA TTCTCGCAAG GCATGGCGGT ACCTGTGTC CCTGTCTTC CCGGGCGGC GAAGCCCCG GGCCTTTTC GTCCGGGTC

1 M etGlulnAr gglyGlnAsn AlaProAla laSerGlyAl aArgLysArg HisGlyProGly

201 GACCCAGGA GCGCGGGG GCGCGGGCT GCGTCCGGT CCCCAGACC CTTGTCTCTG TGTCTGGCG GGTCTGTCTG TTGTCTCTG CTAAGTCTGC  
CTGGTCTCT CCGCGCCCT CCGTCCGAC CCGAGGCCCA GGGTCTCTG GAACACGAG AACAGGGCG CCAGGACGAC AACAGAGTC GACTCAGACG

22 ProArgG1 uAlaArgGly AlaArgProG lYLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValserA laGluSerAla

301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCACAAAC AAAGAGGTC CAGCCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC  
AGACTAGTGG GTTGTCTG ATCAGGGGGT CGTCTCTG CCGGGGTGTT TTTCTCTCCAG GTCCGGGAGT CTCCTTAACA CAGGTGGACC TGTGGTATAG

55 LeuileThr GlnGlnAspL euAlaProG1 nGlnArgAla AlaProGlnG lNlysArgse rSerProser GluGlyLeuC ysProProG1 yHisHisile

401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTCTCTCTT CCGCTGCACC AGGTGTGATT  
AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTAAGTGGAG AAAAGACGAA CCGGACGTGG TCCACACTAA

88 SerGluAspG lyArgAspCy sileSerCys LysTyrglyG lNAspTyrse rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCGAAG AAGGCACCTT CCGGGAAGAA GATTCTCTG AGATGTGCGG  
GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTACACA GTACCGCTTC TTCCGTGGAA GGCCTTCTT CTAAGAGGAC TCTACACGGC

122 GlyGluVa lGluLeuser ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg

601 GAAGTGCCCG ACAGGGTGTG CCAGAGGGAT GGTCAAGTTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA  
CTTCACGGCG TGTCCACAG GGTCTCCCTA CCAGTTCAG CCACATAACAT GTGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT

155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpse rAspIleGlu CysValHisL ysGluSerG1 yIleIleIle

701 GGAGTACACG TTGACGGCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCA GTCTTTACTG TGAAGAAG TCCTTCTCTTA CCTGAAGGC ATCTGCTCAG  
CCTCAGTGC AACGTGGCA TCAGAACTAA CACCGACACA AACAAAGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCG TAGACGAGTC

188 GlyValThrV alAlaAlaVa lValLeuile ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly

FIG. 8A-1



801 GTGGTGGTGG GGACCCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC AGCCCAACCA  
 CACCACCACC CCTGGGACTC GCACACCTGT CTTGAGTGT TCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT  
 222 GlyGlyGly yAspProGlu ArgValAspA rgSerSerG1 nArgProGly AlaGluAspA snValLeuAs nGluIleVal serIleLeuG InProThrGln  
 901 GGTCCTCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA  
 CCAGGGACTC GTCCCTTACC TTCAGGTCCT CGGTCGTCTC GGTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT  
 255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alasnMetLe uSerProGly GluSerGluH isLeuLeuG1 uProAlaGlu  
 1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTTCGA TGACTTTTGA GACTTGGTGC  
 CGACTTTCCA GAGTCTCCTC CTCCGACGAC CAAGGTCGTT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAAGCT ACTGAAACGT CTGAACCCACG  
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG IncysPheAs pAspPheAla AspLeuValPro

**FIG.-8A-2**

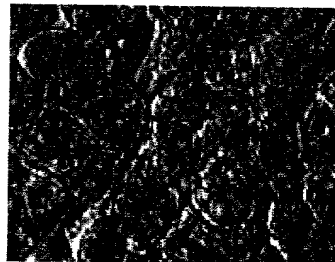
1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCACAGGG ACACCTTGTA  
 GGAACCTGAG GACCCCTGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTCC ACCGATTTCG ACTCCGTCCG CCGGTGTCCC TGTGGAACAT  
 322 PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysV alAlaLysAl aGluAlaAla GlyHisArga spThrLeuTyT  
 1201 CACGATGCTG ATRAAAGTGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCTCTCT GGATGCCCTTG GAGACGCTGG GAGACAGACT TGCCAAGCAG  
 GTGCTACGAC TATTTACACC AGTTGTTTTG GCGCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAAC CTCTGCGACC CTCTCTCTGA ACGGTTCTGC  
 355 ThrMetLeu IleLysTrpV alasnLysTh rGlyArgasp AlaserValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln  
 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA  
 TTCTAACTCC TCGTGAACAA CTCGAGACCT TTCAAGTACA TACATCTTCC ATTACGTCTG AGACGGAAAC GGATTCTACAC TAAGAGAAGT CCTTCACTCT  
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluG1 yAsnAlaasp SerAlaXqqS erOC  
 1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC  
 GGAAGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCITTTGAGAG  
 1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTCTAACTT TTCACTGCAC TTGGCATTTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT  
 GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AATAATATTCG ACTTACACTA TTATTCTCTG GATACCTTTA  
 1601 GTCTGGATCA TTCCGTTTGT GGTACTTTG AGATTGTTT TGGGATGTCA TTGTTTTTTC AGCATTCTT TATCTTAATG TAAATGCTTT ATTTATTAT  
 CAGACCTAGT AAGGCAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTCAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA  
 1701 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAG GCGGCGCCGC ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC  
 AACCCTAGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CCGTACCGG

FIG.-8B

1 MEORGONAPAA SGARKRHGPGPREARGARGLRVPKTLVLVVAALLLVSAESALITQQD  
 61 LAPQORAAFPQKRSSPSEGLCPFGHHI SEDGRDCISCKYQDYSTHWNDLLFLCLRCTRCD  
 121 SGEVELSPCTTTRNTVCCQCEGTFREEDSPEMQRKCR TGCPRMVKVGDCTPWSDI ECVH  
 181 KESGIIIGVTVA AVVLIVAVFVCKSLIMKKVLPYLKGI CSGGGDPERVDRSSQRPGEAD  
 241 NVLNEIVSILQPTQVPEQEMEVEQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRRLLVPA  
 301 NEGDPTELRQCDDFDADLVPFDSWEPLMRKLGMDNEIKVAKAEAGHRDITLYTMLIKW  
 361 VNKTGRDASVHTLLDALETGLERLAKQKIEDHLLSSGKFMYLEGNADSALS

FIG.-9

Vector



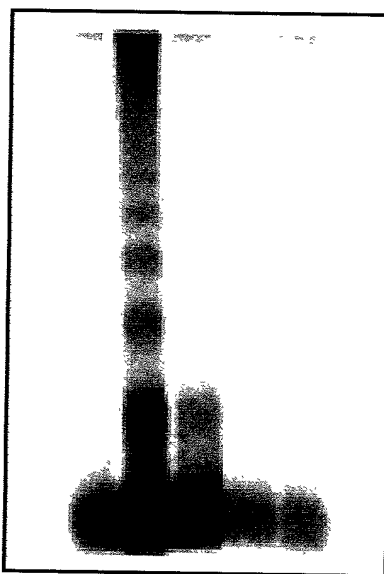
Apo2



Apo2+CrmA



**FIG. 11A**



Vector

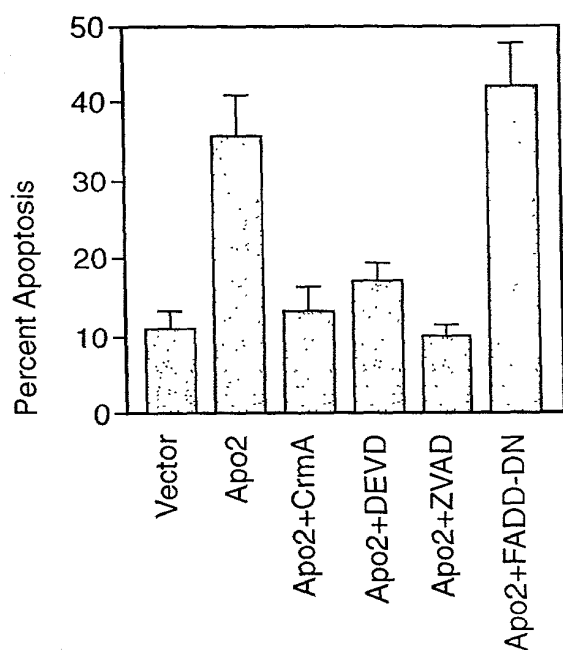
Apo2

Apo2+CrmA

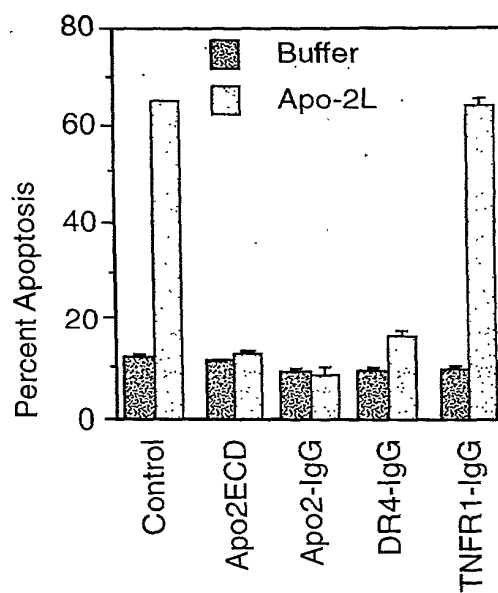
Apo2+DEVD

Apo2+ZVAD

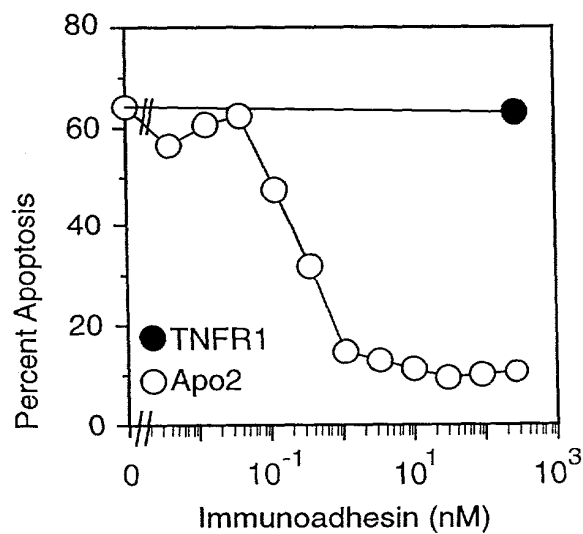
**FIG. 11B**



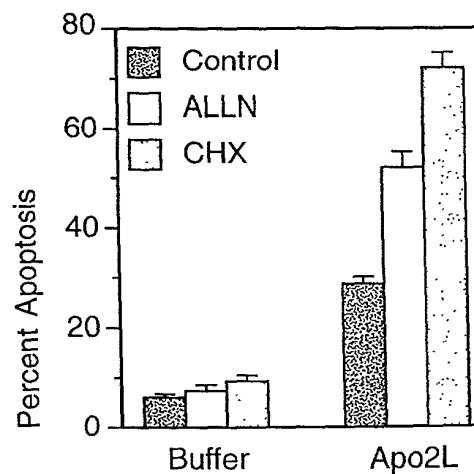
**FIG. 11C**



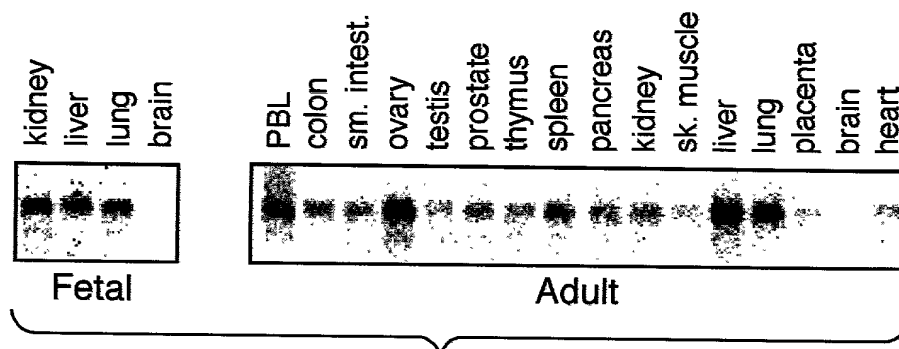
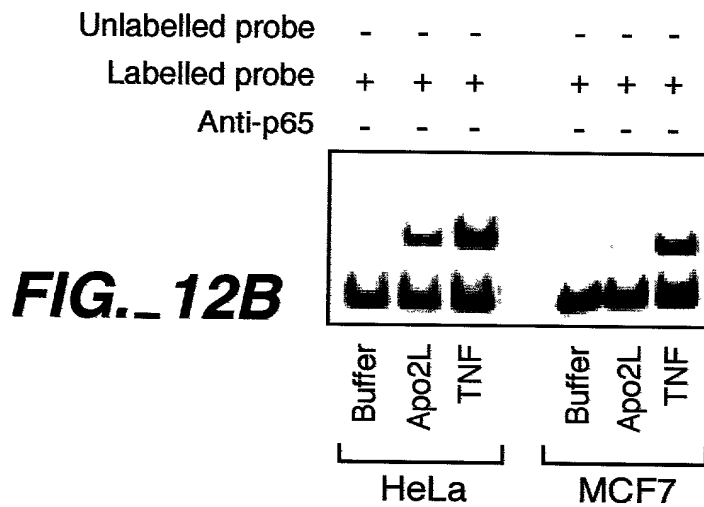
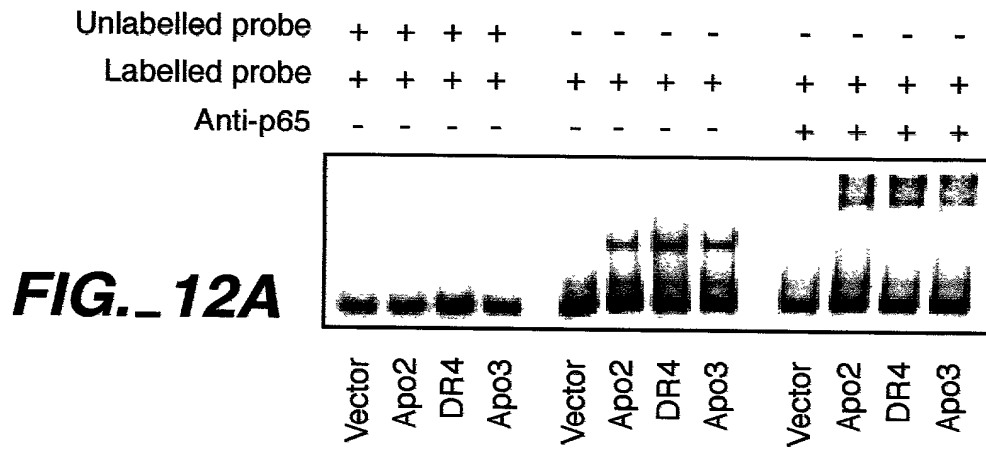
**FIG. 11D**



**FIG. 11E**



**FIG. 12C**



**FIG.\_13**